SUBSTITUTE SHEET

PF-0027 US



SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Coleman, Roger Bandman, Olga Wilde, Craig G.
- (ii) TITLE OF THE INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: U.S.
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/390,740
 - (B) FILING DATE: February 17, 1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Luther, Barbara J.
 - (B) REGISTRATION NUMBER: 33,954
 - (C) REFERENCE/DOCKET NUMBER: PF-0027 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-852-0195
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Human Pancreas
 - (B) CLONE: 223187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAGGTCT	CCGCAGCACT	TCTGTGGCTG	CTGCTCATAG	CAGCTGCCTT	CAGCCCCCAG	60
GGGCTCACTG	GGCCAGCTTC	TGTCCCAACC	ACCTGCTGCT	TTAACCTGGC	CAATAGGAAG	120
ATACCCCTTC	AGCGACTAGA	GAGCTACAGG	AGAATCACCA	GTGGCAAATG	TCCCCAGAAA	180
GCTGTGATCT	TCAAGACCAA	ACTGGCCAAG	GATATCTGTG	CCGACCCCAA	GAAGAAGTGG	240
GTGCAGGATT	CCATGAAGTA	TCTGGACCAA	AAATCTCCAA	CTCCAAAGCC	P	291

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Human Pancreas
 - (B) CLONE: 223187
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala 1 10 15

Phe Ser Pro Gln Gly Leu Thr Gly Pro Ala Ser Val Pro Thr Thr Cys 20

Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser 40

Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe 50

Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp 65

Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys 85

Pro

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Human Pancreas
 - (B) CLONE: 226152
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCAGG 60 ACCCAAGGCA GTGATGGAGG GGCTCAGGAC TGTTGCCTCA AGTACAGCCA AAGGAAGATT 120

CCCGCCAAGG	TTGTCCGCAG	CTACCGGAAG	CAGGAACCAA	GCTTAGGCTG	CTCCATCCCA	180
GCTATCCTGT	TCTTGCCCCG	CAAGCGCTCT	CAGGCAGAGC	TATGTGCAGA	CCCAAAGGAG	240
CTCTGGGTGC	AGCAGCTGAT	GCAGCATCTG	GACAAGACAC	CATCCCCACA	GAAACCAGCC	300
CAGGGCTGCA	GGAAGGACAG	GGGGGCCTCC	AAGACTGGCA	AGAAAGGAAA	GGGCTCCAAA	360
GGCTGCAAGA	GGACTGAGCG	GTCACAGACC	CCTAAAGGGC	CA		402

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Human Pancreas
 - (B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met 1	Ala	Gln	Ser	Leu 5	Ala	Leu	Ser	Leu	Leu 10	Ile	Leu	Val	Leu	Ala 15	Phe
Gly	Ile	Pro	Arg 20	Thr	Gln	Gly	Ser	Asp 25	Gly	Gly	Ala	Gln	Asp 30	Cys	Cys
Leu	Lys	Tyr 35	Ser	Gln	Arg	Lys	Ile 40	Pro	Ala	Lys	Val	Val 45	Arg	Ser	Tyr
Arg	Lys 50	Gln	Glu	Pro	Ser	Leu 55	Gly	Cys	Ser	Ile	Pro 60	Ala	Ile	Leu	Phe
Leu 65	Pro	Arg	Lys	Arg	Ser 70	Gln	Ala	Glu	Leu	Cys 75	Ala	Asp	Pro	Lys	Glu 80
Leu	Trp	Val	Gln	Gln 85	Leu	Met	Gln	His	Leu 90	Asp	Lys	Thr	Pro	Ser 95	Pro
Gln	Lys	Pro	Ala 100	Gln	Gly	Cys	Arg	Lys 105	Asp	Arg	Gly	Ala	Ser 110	Lys	Thr

Gly Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
115
120
125
Gln Thr Pro Lys Gly Pro
130

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Val Ser Ala Ala Leu Leu Ala Leu Leu Leu Leu Ile Ala Ala Ala 1 10 15

Phe Cys Pro Gln Gly Leu Ala Gln Pro Asp Gly Val Asp Thr Pro Thr 20

Thr Cys Cys Phe Asn Tyr Ile Asn Arg Lys Ile Pro Arg Gln Arg Leu 40

Glu Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Ser Lys Pro Ala Val 50

Ile Phe Lys Thr Lys Arg Ala Lys Gln Val Cys Ala Asp Pro Lys Glu 65

Lys Trp Val Gln Asp Ser Met Lys His Leu Asp Lys Gln Thr Pro Lys 90

Pro

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: MIP-la
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala 1 5 10 15

Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala 20 25 30

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala 35

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe 50 55

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
65 70 75 80

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
85 90

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: MIP-1b
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

 Met
 Lys
 Leu
 Cys
 Val
 Thr
 Val
 Leu
 Ser
 Leu
 Met
 Leu
 Val
 Ala Ala 15

 Phe
 Cys
 Ser
 Pro
 Ala Leu
 Ser
 Ala Pro
 Met
 Gly
 Ser
 Asp
 Pro
 Pro
 Pro
 Pro
 Thr
 Thr
 Ala Arg
 Lys
 Leu
 Pro
 Arg
 Asn
 Phe
 Val
 Val
 Asp
 Leu
 Cys
 Ser
 Gln
 Pro
 Arg
 Asn
 Phe
 Val
 Val
 Asp
 Pro
 Arg
 Ser
 Gln
 Val
 Cys
 Ala Asp
 Pro
 Ser
 Glu
 Ser

 Phe
 Gln
 Thr
 Lys
 Gln
 Val
 Cys
 Ala Asp
 Pro
 Ser
 Glu
 Ser

 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser
 From Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: RANTES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Val Ser Ala Ala Arg Leu Ala Val Ile Leu Ile Ala Thr Ala 1 5 10 15

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro 20 25 30

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys 35 40 45

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe 50 55 60

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp 65 70 75 80

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser 90

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: MCP-1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr 85 90 95
Pro Lys Thr

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: MCP-2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: MCP-3
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

 Met
 Trp
 Lys
 Pro
 Met
 Pro
 Ser
 Pro
 Ser
 Asn
 Met
 Lys
 Ala
 Ala
 Ala

 Leu
 Leu
 Leu
 Leu
 Thr
 Ala
 Ala
 Ala
 Pro
 Pro
 Gln
 Gly
 Leu

 Ala
 Gln
 Pro
 Val
 Gly
 Ile
 Asn
 Thr
 Ser
 Thr
 Thr
 Cys
 Cys
 Tyr
 Arg
 Pro

 Ile
 Asn
 Lys
 Lys
 Ile
 Pro
 Lys
 Glu
 Ala
 Val
 Ser
 Tyr
 Arg
 Thr

 50
 Thr
 Ser
 His
 Cys
 Pro
 Arg
 Glu
 Ala
 Val
 Ile
 Phe
 Lys
 Thr
 Lys
 Leu

 65
 Thr
 Ser
 Fro
 Thr
 Gln
 Lys
 Trp
 Val
 Gln
 Asp
 Phe

 85
 Thr
 Thr
 Gln
 Thr
 P